Cell-Based cAMP Assay

180

Figure 1

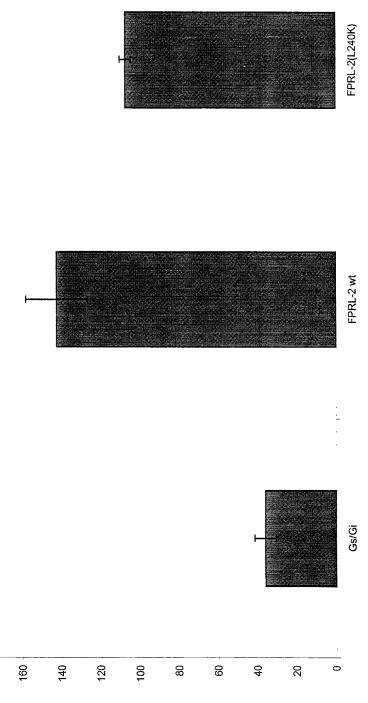
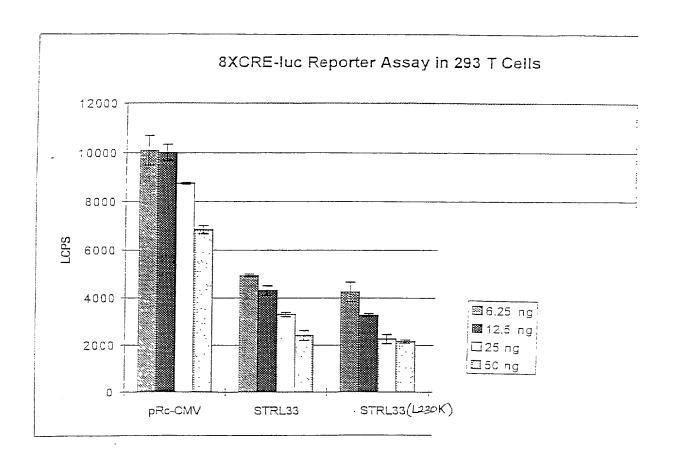


Figure 2



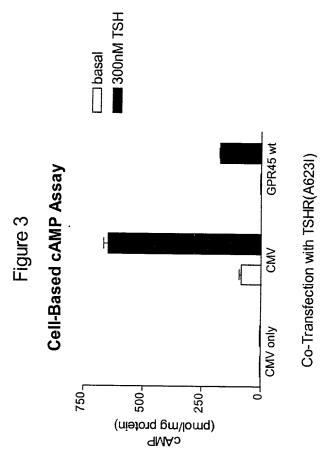
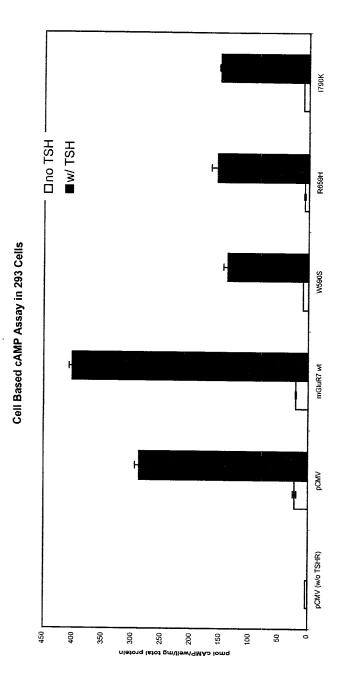


Figure 4



Co-Transfection with TSHR(A623I)

Whole Cell cAMP Assay in RGT Cells 17 5 ■ TSH 15.0_ 12.5. cAMP(pmol/mg protein) 10.0. 7.5_ 5.0. 2.5. 0.0 CMV (w/o TSHR)

Co-Transfection with TSHR(A623I)

W590S

R659H

1790K

Figure 5

mGluR7 wt

CMV

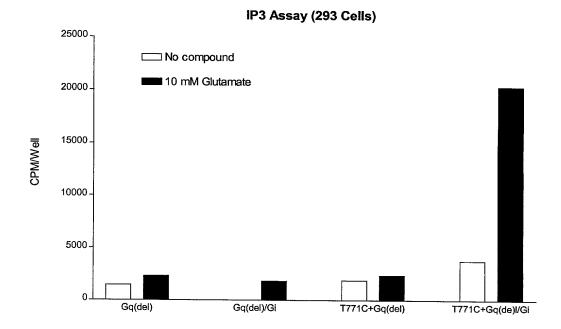


Figure 6

SRE Reporter Assay

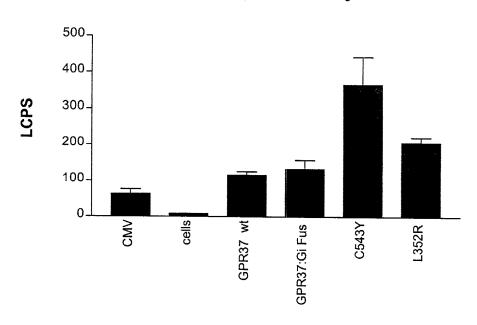
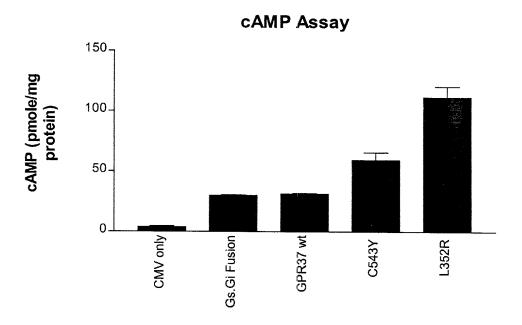


Figure 7



Co-transfection with Gs/Gi Fusion

Figure 8

Northern Analysis of GPCR GPR37 expression in forskolin treated Rat Schwann cells



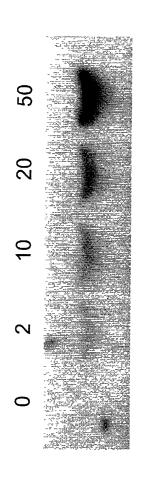
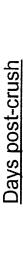


Figure 9

Expression in Crushed Rat Sciatic Nerve Northern Analysis of GPCR GPR37



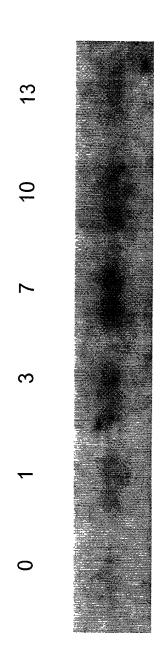
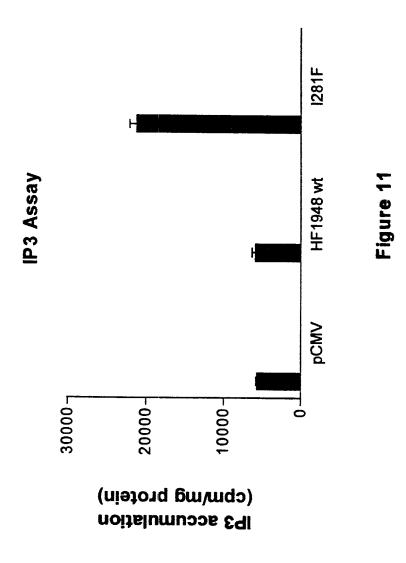


Figure 10



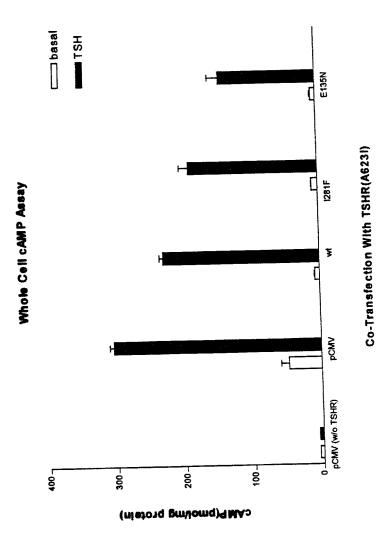
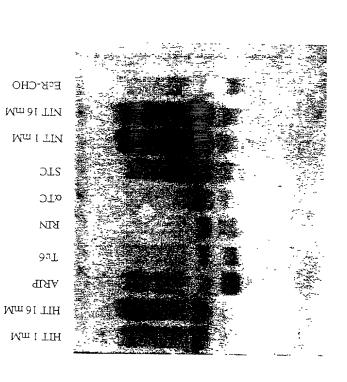


Figure 12

Figure 13

Cell-specific expression of GPRUS variants in pancreatic cell lines



E2F-Luc activation by GPR35 in 293A cells

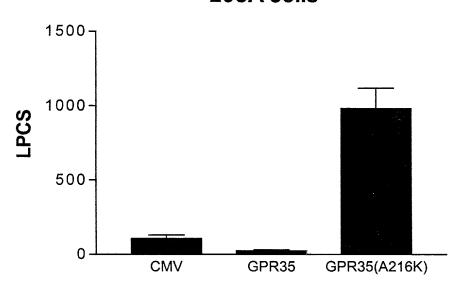
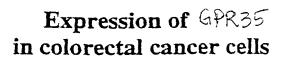
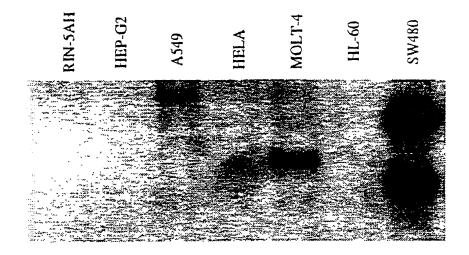


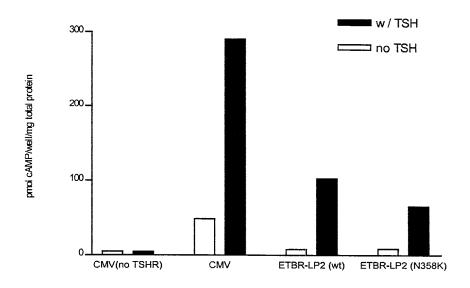
Figure 14

Figure 15





Adenylate Cyclase Assay



Co-Transfection with TSHR(A623I)

Figure 16

AP1 Reporter Assay in 293T Cells

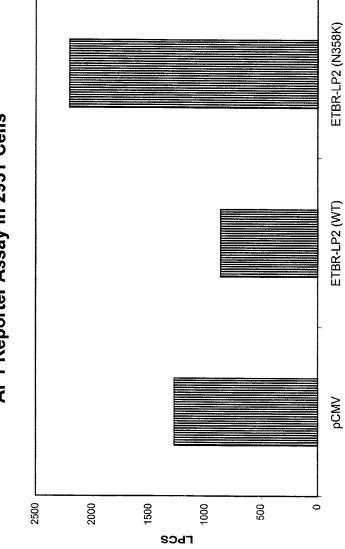


Figure 17

Northern Analysis of ETBR-LP2 in Forskolin Treated Rat Schwann Cells

uM Forskolin

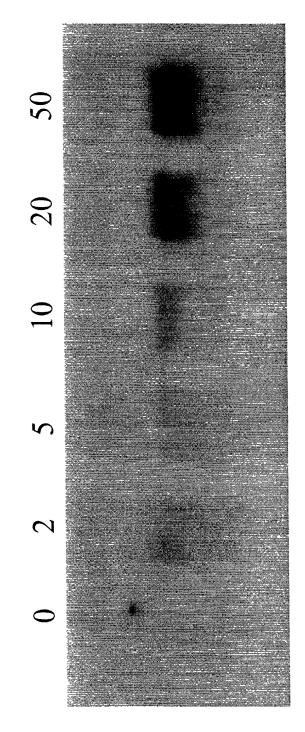


Figure 18

Northern Analysis of ETBR-LP2 Expression in Crushed Rat Sciatic Nerve

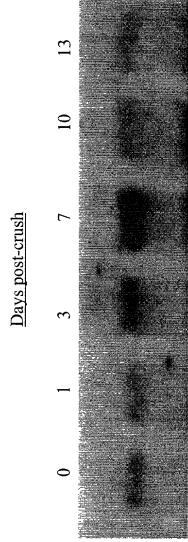
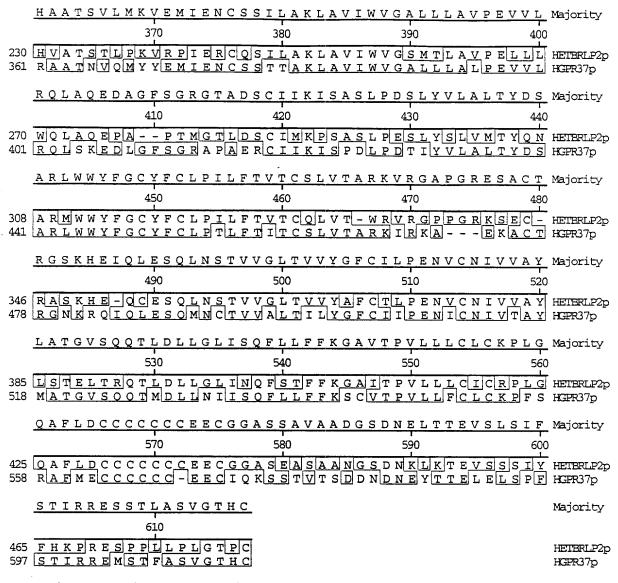


Figure 19

Figure 20A

	MRALGALAAS	LAVLLAVG	•	ALGVGPASRNE	TCL Majority
1 1	M R W L W P L A V S M R A P G A L L A R	LAVILAVG	LSRVSGGA	30 PLHLG ALGVAPASRNE	40 HETBRLP2p
				LRARAETEEQG	
32	50)	60	70 - R H R A F T O F O O	80
41				LRARAPREEOG	AAF HGPR37p
42	90		100	AGPPGPPTRPP	GPW Majority 120
43 81	LAGPSWDLPA	APGRDPAA	GRGAEASA	AGPPGPPTRPP	HETBRLP2p GPW HGPR37p
	RWKGARGTEP		PTALQLFL 140	QISDEEAKGVQ 150	GAG Majority
43 121	RSKRGTE- RWKGARGQEP	 SETLGRGN	PTALOLFL	DEEAKGVO OISEEEEKGPR	LIETTODI DO
		QTVPGASA	LFYRPIHA	GGLQGSННКРL	-
58 161		OYVPEEWA	180 EYPRPIHP	190 AGLQPT KPL GKLOGSHHKPL	VAT HETBRLP2p
				GGIHEPGGPRR	_
86	SPNPDKDGG-	TPDSG	220 QELRGNLT	230 GA PG	240 HETBRLP20
201	ANGLAGHEGW	TIALPGRA	LAQNGSLG	E <mark>GIHEPGGPRR</mark> LAVVVFGVGIV	GNS HGPR37p
112	250	•	260	270	280
241	TNRRVRLKNP	FIY PLTQES	YGAYAVM C	LALVVFAVGIV LSVVIFGTGII	GNL HGPR37p
	AVMCIVWHSY 290		LLASLALWI 300	OFLVLFFCLPL 310	VIF Majority 320
150 281	SVMCIVWHSY AVMCIVCHNY	Y L K S A W N S Y M R S I S N S	ILASLALW LLANLAFW	D F L V L F F C L P I D F L I I F F C L P L	V I F HEIBRLP2p V I F HGPR37p
	NELTKQRLLG 330		FIEVASLGY	VTTFSLCALGI 350	DRF Majority
190 321	NEITKORLLG HELTKKWLLE	DVSCRAVP DFSCKIVP	FMEVSSIG	VTTFSLCALGI VTTFTLCALCI	D. D. El TEMPOR PO-

Figure 20B



Decoration 'Decoration #1': Box residues that match the Consensus exactly.

Decoration 'Decoration #2': Box residues that match the Consensus exactly.